



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number:

TO: Terra Gibbs
Location: CM1/12A12/11E12
Art Unit: 1635
Tuesday, June 24, 2003

Case Serial Number: 998667

From: Mary Jane Ruhl
Location: Biotech-Chem Library
CM1-6A06
Phone: 605-1155

maryjane.ruhl@uspto.gov

Search Notes



From: Gibbs, Terra
Sent: Wednesday, June 18, 2003 12:46 PM
To: "STIC-Biotech/ChemLib"
Subject: Sequence search request...

Could you please do a regular search of SEQ ID NO: 2 of USSN 09/998667?

Thank You!

Terra Gibbs
AU 1635
306-3221
Mailbox: 11E12

ivary Jane Ruhl
Tech. Info. Specialist, STIC
TC-1600
CM-1, Room 6A-06
Phone: 605-1155



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Printed on 12/20/21 HC

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Appendix A

Notes:

APU002'1 HC

Abstract

April 7, 1964

[illegible]

ALL INFORMATION CONTAINED
HEREIN IS UNCLASSIFIED

ACCT 201

5-1-87 11:00

[illegible]

ALL INFORMATION CONTAINED HEREIN IS UNCLASSIFIED

AT 06-07-08

ALICE

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AL450347 III

AL35751: HC

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1	1033:	contig of 1033 bp in length
1034	1133:	gap of 100 bp
1134	5795:	contig of 4662 bp in length
5796	5895:	gap of 100 bp
5896	10386:	contig of 4491 bp in length
10487	10486:	gap of 100 bp
10487	15318:	contig of 4832 bp in length
15319	15418:	gap of 100 bp
15419	19106:	contig of 3688 bp in length
19107	19478:	gap of 100 bp
19207	126620:	contig of 6414 bp in length
25621	25720:	gap of 100 bp
25721	31795:	contig of 6075 bp in length
31796	31935:	gap of 100 bp
31896	38072:	contig of 6177 bp in length
38073	38172:	gap of 100 bp
38173	47433:	contig of 9261 bp in length
47434	47533:	gap of 100 bp
47534	54692:	contig of 7159 bp in length
54693	54702:	gap of 100 bp
54793	60696:	contig of 14277 bp in length
60697	61697:	gap of 100 bp
61697	82605:	contig of 19336 bp in length
82606	82706:	gap of 100 bp
82706	94890:	contig of 13185 bp in length
94891	94991:	gap of 100 bp
95991	106707:	contig of 10717 bp in length
106708	106807:	gap of 100 bp
106808	124545:	contig of 17738 bp in length
124546	124615:	gap of 100 bp
124616	166218:	contig of 41573 bp in length

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            /clone="RP1-5316"  
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[illegible]

Query Match	Score	DB 2,	Length
44.48;	900.8;	DB 2,	166218

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Matches 926; Conservative 0; Mismatches 42; Indels 0; Gaps 0
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1044 AAGACATCTCTAATTACTACACTTTCTTTATGCTGTTTCATAGAGTAAATATAT 1121

Db 69417 TATACTATTGACTCTGAATATTCTAATTATTTTCTTATTTGTAAGATTTAATATAAT 69418

TGAGGGATCTTAAATAATTGAAGAAGTTAATTAATGATCGC

.....

1184 GAACACCACATTAATTTATTTAAAAAGGAGGAAAGGACCACTGAAATTCACCAATTTAA 124

69537 GACACCCATTAATTTCAAAAGAAAGAAAGAACCACTGAATTGACTTTAA 695

1944 GATGCTGTGGACAAAGCGAGCGGAATTGGTAAATGAAATGGGTAATAAATTTGATCAACA 1200

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[illegible]

1004 ACASTA BOSTON ST. BOSTON, MASS. 02116

6965' ACAAATTATGTGTTTCTTAATTTATAAAGTGGTTTAATTTA 6970

1364 ATGGTTTAAATCTGTTTAAATCTTGAGATCTTTAAACATCTTAAACAAACAAATTTA 1421

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1474 TCTACATCAAGTATTGTGTTAAATGGAAAACAACCGTGTAAGCAGAACATATTC

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Db 69777 TCTACATCAGTCATTGTTACATGGAAGAACAAGTAACTAGTGTGAAAGTAATCT 698

1484 GGTTCGAAATTAGTAAATACCTCTGCTATTAATCTTACATATCTAATAATTAGCATCATCG 154

[illegible][illegible]

QY 1544 TTAGGCACGATACTAATCTTGTCTCTGTAAGAAATATCGAGAAGTTAAAT AAAATTCT 1610

69847 TTAGGCAAGAACTAATCTTTGTCTCTGTAATAAAAAATATGGAGAGTGAACCAAGTGC 699

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[illegible][illegible]

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70017 AGCTTAATAATTCTATGCGAGTTG;AAAGAAATTTCGAACTCAAGAAAGTCCATT 700

174 TAAAGGCGGAACCTTCAATTTAATAATTAATTGTAAGTGTATGGC 178

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70127 GATCGACAAAGTTTACGGAGTGTAATACTAAGGTCGTGAAGAATGTTTCTGTGAAAATTCCGT 701

1844 TTTTAAATCTGTAAGATACTCTCAATTCTATATATCATCTAAT 190

[illegible]

1. The first step is to identify the problem or question that needs to be answered. This involves understanding the context and the specific requirements of the task.

(c) TGGAGGCTTGAAGCAAAATTTCTAAGCTTGTGACCTGGTAATTATTCATGCTCAGCGGCA

DB	70267	TTCATGCTAGCCTACGTAACAATATTGAACCTCCCGGAGCGAAGGTAAAGCGTCA	70393
CY	17644	GATGGCGCGCATATCATTTAGCTTGCGTAAAAGAGGTAGATTCATTCAAAAA	2223
DB	70317	GATGCTACTATATAATATTAAGCTTAGCGTAAATAGCGTAACTTCATTCAAAAA	70393
CY	2084	AAAAAAAAA	2031
DB	70377	AAAAAAAAA	70384
RESULT 5			
A0011825			
DEFINITION	Homo sapiens chromosome 19, clone FRI-5316, complete sequence.		
VERSION	A0011825.1		
KEYWORDS	HTG.		
SOURCE	Homo sapiens		
ORGANISM	Homo sapiens		
EXTRACT	Eukaryotic; Chorionic Villus; Vertebrate; Eucelostomi;		
MIMATID	F001614; Primates; Carnivora; Hominoidea; Homo.		
REFERENCE	1. Bases 1 to 176222		
AUTHORS	Britten,B., Nusbaum,C. and Lander,E.		
JOURNAL	Unpublished		
REFERENCE	2. Bases 1 to 176222		
AUTHORS	Britten,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M., Baldwin,J., Barna,N., Beckley,R., Boguski,V.L., Bouckgeater,F., Brown,A., Castle,A., Colangelo,M., Collins,S., Collinge,A., Cozzari,P., Dahlmeier,K., Dewar,P., Delling,X., Edelberg,M., Feyle,M., Ferreira,P., Fitzhugh,W., Forrest,C., Funke,R., Gage,D., Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heathford,A., Horton,L., Howland,J.C., Johnson,P., Jones,C., Kamm,L., Karas,A., Klein,I., Lebecky,J., Levy,C., Locke,K., MacDonald,P., Margus,N., McMan,P., McGuck,A., McKernan,K., McLoughlin,J., Meldrum,T., Moran,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., Peterson,K., Pollara,V., Poley,P., Roy,A., Santos,P., Severy,P., Stange-Themann,N., Stojanovic,N., Subramanian,A., Talamas,J., Testaye,S., Tirelli,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X., Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.		
TITLE	Direct Submission		
JOURNAL	Submitted (15-OCT-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA		
REFERENCE	3. Bases 1 to 176222		
AUTHORS	Britten,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguski,V.L., Bouckgeater,B., Cantarella,C., Chang,J., Chazaro,B., Chesepeli,Y., Collins,A., Cook,A., Cooke,P., DeAtellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J., Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,P., Jones,C., Kamat,A., Karas,A., Kelly,C., Landers,T., Levine,P., Lindblad-Toh,K., Liu,Q., Maclean,C., MacDonald,P., Major,J., Matthews,K., McCarthy,M., Meldrum,T., Meneses,L., Milova,T., Menga,V., Murphy,T., Naylor,J., Nguyen,C., Nishi-Fukuda,Y., O'Connor,T., O'Donnell,P., O'Neill,P., Oliver,I., Peterson,K., Phunkant,P., Pierre,N., Raymond,C., Petta,P., Plise,C., Piggy,P., Roman,J., Roy,A., Schauer,S., Schnuppack,R., Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Themann,N., Stojanovic,N., Talamas,J., Testaye,S., Theodore,D., Thompson,K., Travers,M., Vassiliev,H., Vital,J., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zalcoun,J., Zembek,L., Zimmer,A. and Zody,M.		
TITLE	Direct Submission		
JOURNAL	Submitted (Dec-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA		
REFERENCE	4. Bases 1 to 176222		
AUTHORS	Britten,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguski,V.L., Bouckgeater,B., Cantarella,J., Chang,J., Chazaro,B., Chesepeli,Y., Collins,A., Cook,A., Cooke,P., DeAtellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J., Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,P., Jones,C., Kamat,A., Karas,A., Kelly,C., Landers,T., Levine,P., Lindblad-Toh,K., Liu,Q., Maclean,C., MacDonald,P., Major,J., Matthews,K., McCarthy,M., Meldrum,T., Meneses,L., Milova,T., Menga,V., Murphy,T., Naylor,J., Nguyen,C., Nishi-Fukuda,Y., O'Connor,T., O'Donnell,P., O'Neill,P., Oliver,I., Peterson,K., Phunkant,P., Pierre,N., Raymond,C., Petta,P., Plise,C., Piggy,P., Roman,J., Roy,A., Schauer,S., Schnuppack,R., Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Themann,N., Stojanovic,N., Talamas,J., Testaye,S., Theodore,D., Thompson,K., Travers,M., Vassiliev,H., Vital,J., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zalcoun,J., Zembek,L., Zimmer,A. and Zody,M.		

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TITLE	Direct Submission
Journal	Submitted 24 Nov 2001; Sanger Centre, Hinxton, Cambridgeshire
	20 Feb 2002; Cambridge University Library, Cambridge, UK

COMMENT On Oct 25, 2001 this sequence replaced gi:15858887. During sequence assembly data is removed from overlapping

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VERSION	AL356867.23
KEYWORDS	GI.1865972
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia, Eutheria, Primates, Catarrhini, Hominoidea, Homo, 1 (bases 1 to 147803)
 REFERENCE Ellington, A.
 AUTHORS
 TITLE Direct Submission
 JOURNAL Submitted (12-FEB-2002) Wellcome Trust Sanger Institute, Hinxton,

VECTOR: PCYPAC2


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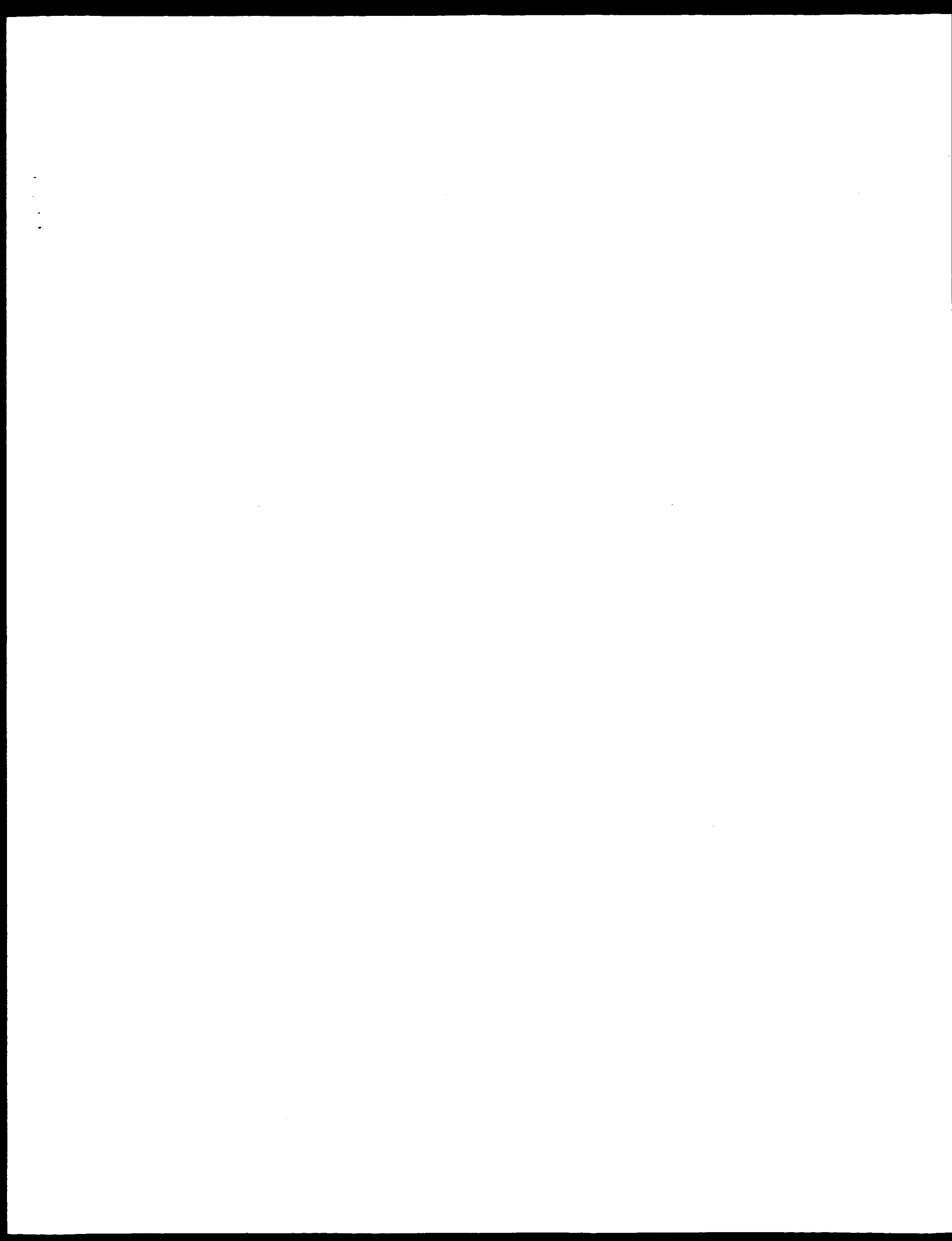
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3 TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
4 TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
5 TITLE OF INVENTION: Sequences Having Internal Fluoresce Binding Sites
6 NUMBER OF SEQUENCES: 44
7 CORRESPONDENT ADDRESS:
8 ADDRESSEE: Puden, Barnett, Moollosky, Smith, Schuster &
9 ADDRESSEE: Russell PA
10 STREET: 200 East Howard Roadward
11 CITY: Fort Lauderdale
12 STATE: FL
13 COUNTRY: USA
14 ZIP: 33301
15 COMPUTER READABLE FORM:
16 MEDIUM TYPE: Floppy disk
17 COMPUTER: IBM PC compatible
18 OPERATING SYSTEM: PC-DOS/MS-DOS
19 SOFTWARE: Patent In Palace # 10, Version #1 25
20 CURRENT APPLICATION DATA:
21 APPLICATION NUMBER: FTT/US94/87726
22 FILING DATE: 15-JUL-1994
23 CLASSIFICATION:
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER: JE 08/037,164
26 FILING DATE: 26-JUL-1993
27 ATTORNEY/AGENT INFORMATION:
28 NAME: Manso, Peter J.
29 REGISTRATION NUMBER: 32,764
30 REFERENCE/DOCKET NUMBER: IN21044-5
31 TELECOMMUNICATION INFORMATION:
32 TELEPHONE: 305-577-2494
33 TELEFAX: 305-764-4996
34 INFORMATION FOR SEQ ID NOS: 33:
35 SEQUENCE CHARACTERISTICS:
36 LENGTH: 15328 base pairs
37 TYPE: nucleic acid
38 STRANDEDNESS: single
39 TOPOLOGY: linear
40 MOLECULE TYPE: CDNA
41 PRT: US94-07926-13

Query Match 10.4%; Score 210.6; DB 5; Length 15328;
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RESULT 5
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Sequence 5, Application US/08629939

GENERAL INFORMATION:
APPLICANT: Kleback, Dirk G.
TITLE OF INVENTION: METHODS FOR DIAGNOSING AN INCREASED
RISK OF PROSTATE CANCER
TITLE OF INVENTION: RISK OF PROSTATE OF OVERALL CANCER
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MICH, ZINN, MACFARLAN & SEARS
STREET: 2100 Pennsylvania Avenue, N.W., Suite 800
CITY: Washington, D.C.
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Palatse #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/92/029,939
FILING DATE: 12-APRIL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KIP, Gordon
REGISTRATION NUMBER: 30,764
REFERENCE/DOCKET NUMBER: A-6612
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 494-7060
TELEFAX: (202) 293-7860
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 320 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO

Query Match	10.38	Score 289.2	DB 17	Length 120
Best Local Similarity	82.68	Pred. No. 56.45		
Matches 245	Conservative	44	Indels 6	Ops 10

	MATCHES	% CONSERVATIVE	% MISMATCHES	Avg. Error Rate
Day 1712 ASMAAUSTCATTAAAGGCGGAATGGCTTCACTTAACCTTTATAACTTGAGAACCAGAACCCGACCATTCCTTTGTGC				

[illegible]

RESULT 6
 US-08-759-873-5/c
 Sequence 5, Application US/08759873
 Patent No. 5681895
 GENERAL INFORMATION.
 APPLICANT: Kieback, Dirk G.
 TITLE OF INVENTION: METHOD FOR FINDING SIMILAR INFORMATION IN A DATABASE
 TITLE OF INVENTION IN BRIEF: METHOD FOR FINDING SIMILAR INFORMATION
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSER: STUBBE, MON, ZIMM, MACPARK & SEAS
 STREET: 2100 Pennsylvania Avenue, N W, Suite 800
 CITY: Washington, D.C.
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20037
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/759,873
 FILING DATE: 12 APRIL 1996
 CLASSIFICATION: 43E
 ATTORNEY/AGENT INFORMATION.
 NAME: Kitz, Gordon
 REGISTRATION NUMBER: 30,764
 REFERENCE/DOCKET NUMBER: A 6612
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 293-7060
 TELEFAX: (202) 293-7860
 INFORMATION FOR SEQ. 13, NO. 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 320 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 HYPOTHETICAL: NO
 US-08-759-873-5
 Query Match: 100%, Score 48.0, DB 1, Length 320,
 Best Local Similarity 82.6%, Pred. No. 5e-45,
 Matches 265; Conservative 0; Mismatches 48; Indels 8; Gaps 2

[illegible]

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1      RESULT 7
2      US-09-033-333-3/C
3      Sequence 3, Application US/09033333
4      Patent No. 6197293
5      GENERAL INFORMATION:
6      APPLICANT: Yu, De Chao
7      APPLICANT: Schuur, Eric
8      APPLICANT: Henderson, Daniel
9      TITLE OF INVENTION: ABEVIVUS VECTORS SPECIFIC
10     TITLE OF INVENTION: FOR TELA EXPRE NDS AND OTHER PROTEIN AND METALS OF COH
11     TITLE OF INVENTION: THEREOF
12     NUMBER OF SEQUENCES 22
13     CORRESPONDENCE ADDRESS:
14     ADDRESSEE: MORRISON & FORSTER
15     STREET: 755 PAGE MILL ROAD
16     CITY: Palo Alto
17     STATE: CA
18     COUNTRY: USA
19     ZIP: 94304-1018
20     COMPUTER READABLE FORM:
21     MEDIUM TYPE: Diskette
22     COMPUTER: IBM Compatible
23     OPERATING SYSTEM: Windows
24     SOFTWARE: FASTSEQ for Windows Version 2.0b
25     CURRENT APPLICATION DATA:
26     APPLICATION NUMBER: 16/09/033,333
27     FILING DATE: 02-MAR-1998
28     CLASSIFICATION:
29     Prior Application DATA:
30     APPLICATION NUMBER:
31     FILING DATE:
32     ATTORNEY/AGENT INFORMATION:
33     NAME: Catherine, Polizzi M
34     REGISTRATION NUMBER: 40,110
35     REFERENCE/DOCKET NUMBER: 34900 000007 00
36     TELECOMMUNICATION INFORMATION:
37     TELEPHONE: 650-913-5600
38     TELEFAX: 650-494-0792
39     TELEX: 706141
40     INFORMATION FOR SEQ ID NO: 3:
41     SEQUENCE CHARACTERISTICS:
42     LENGTH: 5835 base pairs
43     TYPE: nucleic acid
44     STRANDEDNESS: single
45     TOPOLOGY: linear
46     US-09-033-333-3
47     Query Match 10.2%; Score 207.3; Pp 4; Length 5835;
48     Best Local Similarity 72.4%; Fwd 10.34e-44;
49     Matches 252; Conservative 0; Mismatches 48; Indels 6; Gaps 1;

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; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-721-690-1

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Query Match      10 28; Score 207 2; DP 3; Length 5836;
Best Local Similarity 82.4%; Pred. No. 3.4e-44;
Matches 252, Conservative 0, Mismatches 48, Indels 6;
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[illegible]

RESULT 12
 US 08 891 581 1/c
 Sequence 1, Application US/98891581
 Patent No. 618792
 GENERAL INFORMATION
 APPLICANT: Henderson, Daniel R.
 TITLE OF INVENTION: TISSUE SPECIFIC ENHANCER ACTIVE
 TITLE OF INVENTION: IN PROSTATE
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESS:
 ADDRESS: MORRISON & ROBERTSON
 STREET, 795 PACE MILL ROAD
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304-1018
 COMPUTER REPAIR: FORM
 MEDIUM TYPE: Diskette
 COMPUTER: IBM compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEC for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/891.581
 FILING DATE:
 CLASSIFICATION: 514
 Prior Application DATA
 APPLICATION NUMBER: US 08/380,315
 FILING DATE: 10-JAN-1995
 APPLICATION NUMBER: US 08/180,247
 FILING DATE: 13-JAN-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Catherine, FULLEA M
 REGISTRATION NUMBER: 40,110
 REPRESENTATIVE NUMBER: 14882 20001 22
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-813-5600
 TELEFAX: 415-494-0792
 TELFX: 706141
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:

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; LENGTH: 5836 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-891-581-1

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Query Match:	100%	Score: 27.2	Length: 6680
Best Local Similarity	82.48	Pred. No. 3,4e-44	
Matches: 252	Conservative	0	Mismatches: 44
			Indels: 6

[illegible]

RESULT 13
 US-09-033-333-2/C
 Sequence 2, Application US/09033333
 Patent No. 6197293
 GENERAL INFORMATION:
 APPLICANT: Yu, De Qiao
 APPLICANT: Schurr, Eric
 APPLICANT: Henderson, Daniel
 TITLE OF INVENTION: AEROVIRUS VECTORS SPECIFIC
 TITLE OF INVENTION: FOP CELLS EXPRESSING ANTIDOTEN PROTEIN AND METHOD OF USE
 TITLE OF INVENTION: THEREOF
 NUMBER OF SEQUENCES: 22
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORRISON & MORRISON
 STREET: 755 PACE MILL ROAD
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304-1018
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows
 SOFTWARE: Fastseq for Windows Version 2.0b
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/033,333
 FILING DATE: 22 MAR 1998
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATOPREV/ACERT INFORMATION:
 NAME: Catherine, Polizzi; M
 REGISTRATION NUMBER: 40,130
 REFERENCE/DOCKET NUMBER: 34892-20007.00
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-813-5600
 TELEFAX: 650-494-0792

•

•

GenCore version 5.1.6
Copyright © 1993 2003 GenCorp Inc.

Run on: June 23, 2003, 13:32:34, Search time 293 Seconds
(without alignments)
10171.825 Million cell updates/sec

Title: US-09-998-667-2
Sequence: 1 to 33337, chr1:1-13743
Sequence: 1 to 33337, chr1:1-13743

Scoring table:
Gap: 16.0, Gap: 1.0
Scoring: 1642519 swaps, 73171550 residues

Total number of hits satisfying chosen parameters: 2086018

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post processing: Minimum Match: 28
Maximum Match: 100%
Listing first 45 summaries

Database: Published Applications NA:

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2: /cgn2_6/prodata/1/pub/pna/PCOM_NEW_PUB.seq*
3: /cgn2_6/prodata/1/pub/pna/US06_NEW_PUB.seq*
4: /cgn2_6/prodata/1/pub/pna/US07_NEW_PUB.seq*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	1836.4	95.1	4444	10	US-09-998-667-2
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4	1037.6	51.1	1236	9	US-10-017-270-1077
5	765	37.7	765	16	US-09-998-667-4
6	709.6	45.4	1404	18	US-09-998-667-5
7	518.2	25.5	1015	9	US-09-949-842-7
8	220	10.8	684973	10	US-09-263-959-1
9	219.2	10.8	65604	10	US-09-954-631-180
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12	217	10.7	7566	9	US-09-764-891-10010
13	215.2	10.6	16284	9	US-09-764-891-10010
14	214.8	10.6	31474	9	US-09-764-891-10010
15	214.2	10.5	27154	9	US-09-764-891-10010
16	214	10.5	1701	9	US-09-728-552-9
17	213	10.5	6447	10	US-09-764-891-10010
18	213	10.5	16086	10	US-09-764-891-10010
19	213	10.5	169114	9	US-10-067-514-1

20	212.4	10.5	3407	9	US-09-764-891-10010
21	211.6	10.4	2829	9	US-10-116-255-15
22	211.6	10.4	5131	9	US-10-116-255-15
23	211.6	10.4	5131	9	US-10-116-255-15
24	211.6	10.4	5131	9	US-10-116-255-15
25	211.6	10.4	5131	9	US-10-116-255-15
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28	211.6	10.4	5131	9	US-10-116-255-15
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37	210	10.3	714	10	US-09-764-891-10010
38	210	10.3	714	10	US-09-764-891-10010
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[illegible][illegible]

[illegible]

REFERENCE
1 (Pages 1 to 627)
Mammalia, Eutheria: Primates, Catarrhini, Hominoidea.
AUTHORS
NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC).
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strussberg, Ph.D.

Tissue Procurement: ATCC/DC/DT/DTP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: the I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LIML at: imga.jni.gov
Plate: LHC287 row: d column: 07
High quality sequence step: 622

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/clone="IMAGE:3618390"
/clone_1lb="NIH MG-20"
/tissue_type="melanocytic melanoma"
/lab_host="DH10B (phage-resistant)"
/vector="pCR8, Site_1, Xba_1, Site_2"
/ecori_cdna_made_by="oligo-dt printing. Directionally
cloned into EcoRI/XhoI sites using the following 5'
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insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)".
181 a 129 c 145 g 171 t 1 others

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Query Match	23.3%	Score 473.0	DB 10	Length 627
Best Local Similarity	43.4%	Fold No. 1.2e-72		
Matches 479	Conservative	0	Mismatches	4
			Indels	0
			Gaps	0

09 GTTTTCTTACGTAATCAAGGACATATTCTGAACTTTCAGAGTCAATGACATAGGAT 875
 |||||
 10 |||||
 11 |||||
 12 |||||
 13 |||||
 14 GTTTTCTTACGTAATCAAGGACATATTCTGAACTTTCAGAGTCAATGACATAGGAT 901

Dy 876 GGAATATAAAGAAATTGAGAATACAGTGTATCTTCCTTTTGCAAGC 935
|||||
Ddb 202 GGATTAATAAAGAAATTGAGAATACAGTGTATCTTCCTTTTGCAAGC 935
|||||

CY		636	TAAATTATTAAGATACTTGTGATCAATTATTTATTAACATATCAGATCGAAGCGAGG	995
D6		262	TAAATTATTAAGATACTTGTGATCAATTATTTATTAACATATCAGATCGAAGCGAGG	321

Gy 946 CTTGTTGTGGTCACTTGCCGATTAAACCGAATCGAACAGCTTCAGGGGC 105
Db 122 CTGTTGTTGTGTAATTGAGTTTAAATACCGAATCGAACAGCTTCAGGGGC 381

156 AATTAAATAGGAAATCTGTAATTAATCAATTGTTATATGATTCATGATTTT 111
 182 AGTTAATATAGACATCTGCAGTATATCACTTTGTTTATGATGATTCATGATTTT 441

DY 1116 AATVATTATGAGAGTCTTTATCCAAAGCTTAAGACCGGTCACTCTTGAAATATGTC 117
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DB 442 AAATAATATGAGAGTCTTTATCCAAAGCTTAAGACCGGTCACTCTTGAAATATGTC 501

117 AATATCTGAAAGCCGACATATTTTATTAAAGCAAGGCAAGGCAACATGTAATTGCA 123
 |||||
 502 AATATCTGAAAGCCGACATATTTTATTAAAGCAAGGCAAGGCAACATGTAATTGCA 561

cy 1245 CCATTAAAGATGCTGCTTAAACAAATGAGAGAAAGTGTAAATGATTTGAGAGGCAAAA 1294
 Db 562 CCAATTTAAAGATGCTGCTTAAACAAATGAGAGAAAGTGTAAATGATTTGAGAGGCAAAA 620

RESULT
BB287074

LOCUS	848 bp	RNA	linear	EST
BE287074	6010910CSF1	NC1	CGAP_Mams	musculus
ACCESSION	BE287074	RNA sequence.		IMMORT:1485772 5'
VERSION	BE287074.1	GI:9165829		
KEYWORDS				
SOURCE	house mouse.			
ORGANISM	house mouse.			

ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Scuriungathi; Muridae; Murinae; Mus;
1 (bases 1 to 848)
REFERENCE
NIH-MGC <http://mgi.nch.nih.gov/>

URL: <http://www.ncbi.nlm.nih.gov/pmc/articles/PMC1000000/>
 TITLE: National Institutes of Health, Mammalian Gene Collection, (MGC)
 JOURNAL: Unpublished (1999)
 COMMENT: Contact: Robert Strausberg, Ph.D.
 Email: CGA@bhs-remail.nih.gov

Tissue Procurement: Lochat Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (I.M.I.)
DNA Sequencing by: Incyte Genomics, Inc.

phage distribution. MGs clone distribution information can be found through the I M.A.G.E. Consortium/INL at: <http://image.jnl.gov>
 plate: LMA8727 row: 1 column: 13

High quality sequence stop:	1. .848
Location/Qualifiers	
source	
FEATURES	

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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:3465772"
/clone_1ib="NCI_CGAP_Mam5"

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/tissue_type="tumor", gross tissue
/dev stage="7 months"
/lab_host="DHIOB"
/microscopist="Jenny West"
/path="C:\Users\jwest\Documents\Projects\GrossDr
Study\7m07\gross slides\7m07_019.tif"

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190 2 190 7 191 4

ORIGIN	100%	100%	100%
Query Match	22.08	5.09E-446	NP 10; length 848;
Best local similarity	78.78	Ered No. 5.7e-68	

Matches 596; Conservative 0; Mismatches 150; Indels 12; Gaps 5
CY 515 CACCCGAGATGGTAAATTGGTGTCTTTCTTCCTCATCCTTTCTTAAGCGAAGAG 574

[illegible]

61 GGACTGGAGCGGACATATATCTTTGAACTGTTAGTGGTCTGTGAGGAGTATCAACA 120

D6 12 GCGGCTGGGAGACCCGTATGAGTCAAGTGTTCTTGCAGATTCTTAATATATGAGCAGTAGATATAA 18

Gy 695 GAAC---AACCAATGACACTGCTGTAAATATGAGGAGATATCTTCCTTCAAAAATATTC 751

[illegible][illegible]

972 1STAD3ACCACTA*AA3AACTTGAATAA*AA*AA33333TAATTCCTTGGCA 981
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[illegible]

RESULT 8					
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LOCUS	525 bp	mRNA	linear	EST 14 JUL 2000	
DEFINITION	C27G7.1 Y1 NH_MJ_1 Homo sapiens cDNA clone IMAGE 56957,				
ACCESSION	BEJ02781	mRNA sequence:			
VERSION	BEJ02781.1	GI:9186529			
KEYWORDS	EST.				
SOURCE	human.				

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo
; (Accession 1 to 525)
REFERENCE NIH-Webb: hhrp /mgc p01 nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1998)
COMMENT C. H. A. Webb: Strassberg, Ph.D
Email: cga@gs-research.nhl.nih.gov
Tissue Procurement: ARCC/DCTD/DTP
CDNA Library Preparation: Ling Hong/Publn Laboratory
CDNA Library Arrayed by: The I M A G E Consortium (LNL)
DNA Sequencing by: Washington University Genome Sequencing Center
clone distribution: MGC clone distribution information can be
found through the I M A G E Consortium/LNL at:
www.bio.lnl.gov/hhrp/image/image.html
Seq primer: -40RP from Gibco
High quality sequence stop: 513.

FEATURES	Location/Qualifiers
source	1. .525

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/lab_host="PH108 (phage-resistant)"
/note="Organ: skin, Vector: pCRB7, Size: 1 kb, XhoI, Site: 2
EcoRI; cDNA made by oligo-dt priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adapter: GGTACGAG(G) Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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Query Match 20 88; Score 4.0; E-19; Length 525;
Best Local Similarity 99.5%; Pred. No. 7.5e-64;
Matches 424; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DE			
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DE			
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QY	848	GGAAATTGATGAGAAAGAGCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	994
DE			
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DE			
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DE			
QY	1055	CAATTATTAAG	1114
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QY	240	CAATTATTAAG	399
DE			
QY	1115	TAACTGAATGAG	1174
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QY	400	TAACTGAATGAG	459
DE			
QY	1175	GAATGAG	1234
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QY	460	GAATGAG	519
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QY	1235	AGCATT 1240	
DE			
QY	520	ACGATT 525	
DE			

RESULT 9
BI648756
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BI648756 798 bp mRNA EST 12-SEP-2001
K0327075P1.N1_MAF_Mus musculus cDNA clone IMAGE15317267 5'
mRNA sequence.
BI648756
F0148766.1 37:15567932
EST.
house mouse.
Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases) 1 to 798
NIH-NCI http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.

```

Email: CGABgs_tsmail.nhn.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
cDNA Library Preparation: Life Technologies, Inc
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MSC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM1:804 row f column: 20
High quality sequence stop: 764.

Location/Qualifiers
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/dev_stage="10 months"

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19.78; score 399.2; EB 13; length 856;

KEYWORDS
EST.
SOURCE
house mouse.

